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 144
 Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu
 10 35 40 45

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 192
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 15 50 55 60

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 240
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 288
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 gcc gcc gtc tcg gag ttc ggc atc gat ttg gaa gcc gag cgg ctg atc
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 432
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 Lys Ser Asp Asn Tyr Arg Ser Arg Val Val Tyr Glu Pro Arg Ala Val
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 50 165 170 175

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 576
 His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro
 55 180 185 190

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195 200 205

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672

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165 170 175

10 His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro
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15 Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr
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192
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 85 90 95
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 336
 Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val
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 Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln
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 Cys Ser Cys Thr Ala Phe Thr Ile Ile Gly Leu Pro Pro Asp Trp Tyr
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 Trp Asp Thr Thr Ala Asp Thr Arg Tyr Met Val Leu Pro Val Gln Pro
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 ccg gaa acc atc ggc tgg ccc gag gag aaa ctg gtc gac atc gtg acg
 624
 Pro Glu Thr Ile Gly Trp Pro Glu Glu Lys Leu Val Asp Ile Val Thr
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Pro Val Glu Gln Arg Val Asp Ala Ile Gln Ala Ala Leu Asp Glu Arg
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Gly Leu Asn Ala Ser Asp Ala Val Gln Glu Leu Ser His Leu Ala Glu
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Glu Gln Trp Ile Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala Trp
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Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala
85 90 95

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Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val
100 105 110

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Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln
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Cys Ser Cys Thr Ala Phe Thr Ile Ile Gly Leu Pro Pro Asp Trp Tyr
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Lys Asp Leu Glu Tyr Arg Ala Arg Val Val Arg Glu Ser Arg Thr Val
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Leu Lys Glu Met Gly Leu Asp Leu Pro Arg Asp Val Glu Ile Arg Val
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Trp Asp Thr Thr Ala Asp Thr Arg Tyr Met Val Leu Pro Val Gln Pro
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96
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192
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35 gtg ctc gtc gat acc tac gag aac aag atc ggt ccg cga aac ggc gct
240
Val Leu Val Asp Thr Tyr Glu Asn Lys Ile Gly Pro Arg Asn Gly Ala
65 70 75 80

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288
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336
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100 105 110

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384
Gln Gly Glu His Met Val Ala Leu Glu Asn Thr Pro Ala Val His Asn
115 120 125

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432
Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
130 135 140

ctg ccc ccg gtc tgg tac aaa tcg gcg ccc tac cga tcg cgc tcg gtc
480
Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Ser Val
145 150 155 160

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528
Ile Asp Pro Arg Gly Val Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu
165 170 175

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576
Gly Val Glu Val Arg Val Trp Asp Ser Thr Ala Glu Leu Arg Tyr Leu
180 185 190

15 gtt ttg ccg gag cgg ccc gaa ggc acg gcg caa ctg agc gaa gaa gcg
624
Val Leu Pro Glu Arg Pro Glu Gly Thr Ala Gln Leu Ser Glu Glu Ala
195 200 205

20 ctc gcg gat ctc gtc acc cgg gat gcc atg atc ggc gtc gcg aaa gtc
672
Leu Ala Asp Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
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Val Leu Val Asp Thr Tyr Glu Asn Lys Ile Gly Pro Arg Asn Gly Ala
65 70 75 80

Arg Val Val Ala Arg Ala Trp Val Asp Pro Ala Tyr Lys Glu Arg Leu
85 90 95

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Leu Lys Asp Ala Thr Ser Ala Ile Ala Glu Leu Gly Tyr Thr Gly Ala
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Gln Gly Glu His Met Val Ala Leu Glu Asn Thr Pro Ala Val His Asn
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Ile Asp Pro Arg Gly Val Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu
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Gly Val Glu Val Arg Val Trp Asp Ser Thr Ala Glu Leu Arg Tyr Leu
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Val Leu Pro Glu Arg Pro Glu Gly Thr Ala Gln Leu Ser Glu Glu Ala
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96			
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gag aag ggc tat gtc gat ccg gcg gcg ctc gac cgg atc gtc gag gcg			
144			
10	Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala		
	35	40	45
ttc gag acc agg atc ggc ccg cat atc ggc gcc cgt atc gtg gca cgg			
192			
15	Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg		
	50	55	60
gct tgg gcc gac gcc gaa ttc aag cgg cgg ctg ctc gcc gac gcg acc			
240			
20	Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr		
	65	70	75
gag gcg gcg aat tcg ctg ggt cat gcg agc ccg gtc ggc agc cat ctg			
288			
25	Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu		
	85	90	95
atc gcg gtc gag aac acg ccg cag acc cac aac ctc gtc gtc tgc act			
336			
30	Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr		
	100	105	110
ttg tgc tcg tgt tat ccg tgg gag gtg ctg gga ttg ccg ccg gtc tgg			
384			
35	Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp		
	115	120	125
tac aaa tcc gct gcc tac cgc tcg cgc gtg gtg atc gac ccc aag ggc			
432			
40	Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly		
	130	135	140
gtc ctc gcc gag ttc ggc ctg acc ctg cca ccg gag acc ggg atc cgc			
480			
45	Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg		
	145	150	160
atc tgg gat tcg acc gcc gag acc cgg ttt ctg gtg gtg ccg atg cgg			
528			
50	Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg		
	165	170	175
ccc ccc ggc acc gca ggc tgg agc gag gaa cgg ctc gcc gaa ctc gtc			
576			
55	Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val		
	180	185	190
acc cgc gac agc atg atc ggc act ggt ctg gcc ggg gcg ccg cag gag			
624			

Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu
195 200 205

atg gcc tcg gca tga
5 639
Met Ala Ser Ala
210

10 <210> 44
<211> 212
<212> PRT
<213> Unknown

15 <220>
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<400> 44

20 Met Pro Asp Asp His Ala His Pro Asp Asp His Ala His Gly Ser Glu
1 5 10 15

Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr
25 20 25 30

Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala
30 35 40 45

Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg
50 55 60

35 Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr
65 70 75 80

40 Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu
85 90 95

Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr
45 100 105 110

Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp
50 115 120 125

Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly
55 130 135 140

Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg
145 150 155 160

Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg
165 170 175

5 Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val
180 185 190

10 Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu
195 200 205

Met Ala Ser Ala
210

15

<210> 45
<211> 696

<212> DNA

20 <213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M15aA6

25 <220>

<221> CDS

<222> (1)..(696)

<223>

30 <400> 45

atg cgt tcg ccc ggt gag gcc tca gca acg caa cca gcg ctc att cgg
48

Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg
1 5 10 15

35

ctg cat gat cga gct ggc ggc gtt cga tca ttg cgc ggc aaa agg tct
96

Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser
20 25 30

40

cat cgc gcc gga tcg cat cct cgg ggc gct cgc gca tcc gtc gcc aca
144

His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr
35 40 45

45

ggg tgg ttc gtt ccg ttc tcg gcc agg ctc gcc cgg aaa ggc atc gct
192

Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala
50 55 60

50

cct ccg gcc gag atc gcc gag cgg atc gcc gtc acc gat cgc gca tca
240

Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser
65 70 75 80

55

ccg gca atg ggc gct cgc atg gtc gcc aag gcc tgg acc gat ccc gcc
288

Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala
85 90 95

ttc cgc acc ctg ctc ttg gaa gac gga acc cgc gcg gaa tcg ctc
 336
 Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu
 5 100 105 110

 ggc atc atg atg cgc ggc gcc ccg cct ctc ggt gtg ctg gag aat acg
 384
 Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr
 10 115 120 125

 ccc gag att cat cac ctc gtc gtt tgc acg ctg tgc agt tgt tac ccg
 432
 Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro
 15 130 135 140

 cgc gcg gtg ctg ggc tat ccg ccg ttc tgg ttc aaa tcc gcc gcc tac
 480
 Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr
 20 145 150 155 160

 cgg gca cgt gcg gtg cgc gac ccg cgc ggt ctg atc gcc gaa tgg ggc
 528
 Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly
 25 165 170 175

 acc atg ctg ccc gac gat gtc cgc gtg cga gtg gtg gac agt acg gcc
 576
 Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala
 30 180 185 190

 gac tat cgc tgg atg gtt ctg ccg gtg cgg ccg gcc ggc act gcg ggc
 624
 Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly
 35 195 200 205

 tgg gat gag gag cgc ctc gcc gca atc gta cgc gaa ggc gat atg atc
 672
 Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile
 40 210 215 220

 ggg gtg acc atc cct cgt ctt taa
 696
 Gly Val Thr Ile Pro Arg Leu
 45 225 230

 <210> 46
 <211> 231
 <212> PRT
 <213> Unknown

 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M15aA6
 55 <400> 46

Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg
1 5 10 15

Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser
20 25 30

5 His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr
35 40 45

10 Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala
50 55 60

15 Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser
65 70 75 80

20 Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala
85 90 95

25 Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu
100 105 110

30 Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr
115 120 125

35 Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro
130 135 140

40 Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly
145 150 155 160

45 Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala
180 185 190

50 Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly
195 200 205

55 Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile
210 215 220

55 Gly Val Thr Ile Pro Arg Leu
225 230

<211> 576
<212> DNA
<213> Unknown

5 <220>
<223> Metagenome - alpha unit nitrile hydratase - M23dA12

<220>
<221> CDS
10 <222> (1)..(576)
<223>

<400> 47
atg cag ttg cgc gtg cg^g g^c ctg gaa acc gtt cta gcc gaa aag ggt
15 48
Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly
1 5 . 10 15

20 tat ctc gat ccc gcc g^c g^c ctt gat g^c atg atc gaa gcc tac gag acg
96
Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr
20 25 30

25 cg^g att ggg cc^g cat aac gg^c g^c g^c gtc gtc gcc aag gcc tgg tcc
144
Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser
35 40 45

30 gac gcc gca ttc aag cga g^c g^c ctg gtc gag gat g^c acc aag gcc gtg
192
Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val
50 55 60

35 cag tcg ttc ggc gtg gtc aat cg^c gtc ggc gat cac ctg atc g^c g^c gtc
240
Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val
65 70 75 80

40 gag aac acg ccc acg ctg cac aac atc atc gtg tgc acg ttg tgc tcc
288
Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser
85 90 95

45 tgc tat ccg tgg gaa gtg ctc ggc ctg cc^g cc^g gtc tgg tac aaa tcg
336
Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser
100 105 110

50 g^c cc^g tac cg^c tcg cc^g g^c gtc aac gac cc^g cc^g ggg gta ctc gcc
384
Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala
115 120 125

55 gat ttc ggc ctg aag ctg g^c g^c gat atg caa atc cgt gtc tgg gat
432
Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp
130 135 140

tcg acc gcc gag acg cgc ttc atc gtg ttg ccg atg cgc ccg gcc gga
480
Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly
145 150 155 160
5
acc gac ggc tgg agc gaa gaa aag ctc gcc gcg ctg gtg aca cgc gat
528
Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp
165 170 175
10
tgc atg atc ggc acc ggc tta ccc aag caa ccc aac gag gtc acg taa
576
Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr
180 185 190
15
<210> 48
<211> 191
<212> PRT
20 <213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M23dA12
25 <400> 48

Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly
1 5 10 15
30
Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr
20 25 30

35 Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser
35 40 45

Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val
40 50 55 60

Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val
45 65 70 75 80
Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser
85 90 95
50
Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser
100 105 110
55 Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala
115 120 125

Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp

130 135 140

5 Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly
145 150 155 160

10 Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp
165 170 175

15 Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr
180 185 190

20 <210> 49
<211> 624
<212> DNA
<213> Unknown

25 <220>
<223> Metagenome - alpha unit nitrile hydratase - M49bD9

30 <220>
<221> CDS
<222> (1)..(624)
<223>

35 <400> 49
atg agc gag cac gat tcc ggc gaa agc cat cac cat ccg cag cca cta
48 Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu
1 5 10 15

40 tcg cag gcg gca ttg cgc gcg aag gcg atc gaa tcg ctg ctg gtc gaa
96 Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu
20 25 30

45 aag ggg ctg atc gcg acc gac gtg atc gat cgc gtg gta gca acg tac
144 Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr
35 40 45

50 gag aaa gaa gtc ggg ccg ctc aac ggc gct aaa gtc gtc gcg cgg gcc
192 Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala
50 55 60

55 tgg acc gat ccg gag tac cgc cgc aga ctg ctc aag aac ggc acg gcg
240 Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala
65 70 75 80

55 gcg att gcc gag ctg gga ttc ggc ggc ttg cag ggc gaa cac atg atg
288 Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met
85 90 95

gtc gtg gaa aac acg ccg tcc gta cat aac gtg atc tgt tgc acg cta
 336
 Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu
 100 105 110
 5
 tgc tca tgc tat ccg tgg ccg gtc ctg gga ctt ccg ccg agc tgg tac
 384
 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr
 115 120 125
 10
 aag tcg ctg gcg tat cgt tcg cga atc gtg cgc gag ccg cgc gcc gtc
 432
 Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val
 130 135 140
 15
 ctc ggc gaa ttc ggc ctc gaa ttg ccc gaa acg gtg gaa gtc cgc gta
 480
 Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val
 145 150 155 160
 20
 tgg gat agc agt gct gag atg cgc tat ctc gtg ttg ccg gag cgt cca
 528
 Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro
 165 170 175
 25
 gcg gga acg acg gag ttg agc gaa gcg gaa ttg gct tca ttg atc acg
 576
 Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr
 180 185 190
 30
 cgc gat gcc ttg atc ggc gtg gcg aaa gtc gcg gcg cca agc cgc tag
 624
 Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg
 195 200 205
 35
 <210> 50
 <211> 207
 <212> PRT
 40 <213> Unknown
 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M49bD9
 45 <400> 50
 Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu
 1 5 10 15
 50
 Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu
 20 25 30
 55 Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr
 35 40 45
 Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala

50 55 60

5 Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala
65 70 75 80

10 Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met
85 90 95

15 Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu
100 105 110

20 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr
115 120 125

25 Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val
130 135 140

30 Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val
145 150 155 160

35 Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro
165 170 175

40 Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr
180 185 190

45 Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg
195 200 205

50 <210> 51
<211> 600
<212> DNA
<213> Unknown

55 <220>
<223> Metagenome - alpha unit nitrile hydratase - M6dE2
<220>
<221> CDS
<222> (1)..(600)
<223>
<400> 51
atg agc aac cca cgc cgt cga gaa cgg tcg gcc cca ccg gat gcg cga
48
Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg
1 5 10 15

gcc aag gcg ctc gca gaa gcg ctt tcg aag caa gga ctc gtg ccg gaa
 96
 Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu
 20 25 30
 5
 ggg ttc ctc gac cag gtc ggt tct cac gcc gcg gag gcg tgg agc ccg
 144
 Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro
 35 40 45
 10
 cga aac ggc gca cgg gtc gtg gcg cgg gcg tgg gtg gat ccc gag tac
 192
 Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr
 50 55 60
 15
 cgg acg cgc ttg ctc gcc gac ggc acc gcc gcg tgc gcc gcg ctc ggc
 240
 Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly
 65 70 75 80
 20
 tac gcg gga ccg cag gga gag tac atc gtg gta ctc gaa gac acg ctg
 288
 Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu
 85 90 95
 25
 gcc gtt cac aac gtg atc gtg tgt acg caa tgc tcg tgt act gcg tgg
 336
 Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp
 100 105 110
 30
 ccc gtg ctg ggg ctg ccg ccc gat tgg tac aag agt ccg gag tat cgc
 384
 Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg
 115 120 125
 35
 gcc cgc gtc gtg cgg gag ccg cga cgg gtg ctt cgc gaa atg ggc ctc
 432
 Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu
 130 135 140
 40
 gag cta tcc gag agc gtg acg atc cgc gtg tgg gat acg act gcg gaa
 480
 Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu
 145 150 155 160
 45
 acg cgc ttc ctg gtg ctg ccg ctt cgg ccg gcg gga acc gaa ggg tgg
 528
 Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp
 165 170 175
 50
 agc gcg gag cag ctc gcg tcg ctc gtc acg cgc gag gcg atg atc ggc
 576
 Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly
 180 185 190
 55
 gtg gcg cgg gtc gag gtg gtg tag
 600
 Val Ala Arg Val Glu Val Val
 195

5 <210> 52
 <211> 199
 <212> PRT
 <213> Unknown

10 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M6dE2
 <400> 52

15 Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg
 1 5 10 15

20 Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu
 20 25 30

25 Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro
 35 40 45

30 Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr
 50 55 60

35 Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly
 65 70 75 80

40 Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu
 85 90 95

45 Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp
 100 105 110

50 Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg
 115 120 125

55 Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu
 130 135 140

60 Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu
 145 150 155 160

65 Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp
 165 170 175

70 Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly
 180 185 190

Val Ala Arg Val Glu Val Val
195

5
<210> 53
<211> 645
<212> DNA
<213> Unknown

10
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<223> Metagenome - alpha unit nitrile hydratase - M25A18

15
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<221> CDS
<222> (1)..(645)
<223>

20
<400> 53
atg agc ggc acg cat cac cac gac cat gac cac gat cat gac cat gcc
48
Met Ser Gly Thr His His His Asp His Asp His Asp His Asp His Ala
1 5 10 15

25
cat ccg ggc gtc gcc aag gac gag aag gtc cac ggc tat tac caa ttg
96
His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu
20 25 30

30
ctc ggc ctc gcc atc aaa gag ctg ctg atc gaa aaa ggc gtc atc acc
144
Leu Gly Leu Ala Ile Lys Glu Leu Leu Ile Glu Lys Gly Val Ile Thr
35 40 45

35
gcc gcc gag gtg cgc caa gcg atc gag gcg cgc gac gcg atc acg ccg
192
Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro
50 55 60

40
tcg ctc ggc ggc aag gtg gtc gcg cgc gcc tgg acc gat ccg gcc tac
240
Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr
65 70 75 80

45
aag gcg cgg ctg atc gat ccc gcc gcc gac atg atg gag atg ggc
288
Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Ala Met Met Glu Met Gly
85 90 95

50
gtc gat ctc ggc ccc acc gga ctc gcc atc gcc gag aac acg ccg gag
336
Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu
100 105 110

55
gcg cac aac gtc atc gtc acc ctg tgc tcg tat ccg cgc gcc
384
Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala
115 120 125

gtg ctc ggc ctg ccg ccc tcc tgg tac aag gac cgc gat tac cg⁴³²
432
Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser
130 135 140

5 cgc gtg gtg cgc gag ccg cgc gcc gtg ctc aag gag ttc ggc acg gaa
480
Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu
145 150 155 160

10 ttg ccc gac gac gtc gac gtc cgc gtc cac gat tcg acc gcc gat ctg
528
Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu
165 170 175

15 cgc tat ctc gtg ctg ccg atg cgc ccg gcc acc gag ggc atg agc
576
Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser
180 185 190

20 gag gcg gag ctg gcc gag atc gtg acg cgc gac tgc atg atc ggc gtg
624
Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val
195 200 205

25 acg gtg ccg aaa gcg ccc taa
645
Thr Val Pro Lys Ala Pro
210

30

<210> 54
<211> 214
<212> PRT
35 <213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M25A18

40 <400> 54

Met Ser Gly Thr His His Asp His Asp His Asp His Asp His Ala
1 5 10 15

45 His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu
20 25 30

50 Leu Gly Leu Ala Ile Lys Glu Leu Leu Ile Glu Lys Gly Val Ile Thr
35 40 45

55 Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro
50 55 60

65 Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr
70 75 80

Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Met Met Glu Met Gly
 85 90 95
 5

Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu
 100 105 110
 10

Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala
 115 120 125
 15

Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser
 130 135 140
 20

Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu
 145 150 155 160
 25

Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu
 165 170 175
 30

Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser
 180 185 190
 35

Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val
 195 200 205
 40

Thr Val Pro Lys Ala Pro
 210

<210> 55
 <211> 627
 <212> DNA
 <213> Unknown

<220>
 45 <223> Metagenome - alpha unit nitrile hydratase

<220>
 <221> CDS
 <222> (1)..(627)
 50 <223>

<400> 55
 atg agc ggt cac cat cac gac cac gac cat gag cac gac aac cac ttc
 48
 55 Met Ser Gly His His Asp His Asp His Glu His Asp Asn His Phe
 1 5 10 15
 acg ccg atc gaa gcg cgc gtg aag gcg ctg gaa tcg ctg ctg gtc gcc
 96

	Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala		
	20	25	30
5	aag ggc tat gtc gat ccc gcc gcg ctc gat gcg atc atc gac acc tat		
	144		
	Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr		
	35	40	45
10	gag acg aag atc ggc ccg cgc aac ggc gcc cgc gtc gtc gcc aag gcc		
	192		
	Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala		
	50	55	60
15	tgg acc gat ccg gaa ttc gcg gcg cgg ctc aag cag gat ggc agc gcc		
	240		
	Trp Thr Asp Pro Glu Phe Ala Ala Arg Leu Lys Gln Asp Gly Ser Ala		
	65	70	75
20	80		
	gcc gtc gcc gaa ctc ggc tat ggc ggg cgt ggc ggc gag cat atc gtc		
	288		
	Ala Val Ala Glu Leu Gly Tyr Gly Arg Gly Glu His Ile Val		
	85	90	95
25	gac tgt ttc aat acg ccc gaa gag cac aac ctg atc gtc tgc acg ctc		
	336		
	Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu		
	100	105	110
30	tgc tcg tgc tat ccc tgg ccg gtg ctc ggc ctg ccg ccg gtc tgg tac		
	384		
	Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr		
	115	120	125
35			
	aaa tcc ccg ccc tat cgc tcg aaa gcg gtg atc gac ccg cgc ggc gtg		
	432		
	Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val		
	130	135	140
40			
	ctg gcc gat ttc ggc gtg acc ctg ccg gag gga caa agg atc cgc gtc		
	480		
	Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val		
	145	150	155
	160		
45			
	tgg gat tcc acc gcc gaa acc cgc ttc att gtc atc ccc ctg cgc ccg		
	528		
	Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro		
	165	170	175
50			
	gcc ggg acg gaa ggc tgg tcg gaa gaa cag ctg gcg gac gtg acg		
	576		
	Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr		
	180	185	190
55			
	cgt gac agc atg atc ggc acc ggc gtg gtc agc gcg gag gat tcg cga		
	624		
	Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg		
	195	200	205

tga
627

5 <210> 56
<211> 208
<212> PRT
<213> Unknown

10 <220>
<223> Metagenome - alpha unit nitrile hydratase
<400> 56

15 Met Ser Gly His His His Asp His Asp His Glu His Asp Asn His Phe
1 5 10 15

20 Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala
20 25 30

25 Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr
35 40 45

30 Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala
50 55 60

35 Ala Val Ala Glu Leu Gly Tyr Gly Gly Arg Gly Glu His Ile Val
85 90 95

40 Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu
100 105 110

45 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr
115 120 125

50 Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val
130 135 140

55 Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val
145 150 155 160

55 Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro
165 170 175

Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr

180 185 190

5 Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg
195 200 205

10 <210> 57
<211> 696
<212> DNA
<213> Unknown

15 <220>
<223> Metagenome - alpha unit nitrile hydratase - M3aG10

20 <220>
<221> CDS
<222> (1)..(696)
<223>

25 <400> 57
atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc
48 Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr
1 5 10 15

30 ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac
96 Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His
20 25 30

35 cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc
144 Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu
35 40 45

40 gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac
192 Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
50 55 60

45 gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg
240 Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
65 70 75 80

50 cgc gtt gtc gcg ccg gcc tgg gtt gac ccg gac tac aag caa cgg tta
288 Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
85 90 95

55 ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg
336 Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
100 105 110

384 cag ggc gct gac atc ccg gtc gtc gaa aac acg gcc act gta cat aac
Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn

	115	120	125
	ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc		
	432		
5	Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly		
	130	135	140
	ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg		
	480		
10	Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val		
	145	150	155
	atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac		
	528		
15	Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp		
	165	170	175
	cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta		
	576		
20	His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu		
	180	185	190
	gtg ctg ccg gag cgg ccg gcc gga acc aac ctg aca gaa gaa gcg		
	624		
25	Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala		
	195	200	205
	ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc		
	672		
30	Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val		
	210	215	220
	gcg ccg ccg gga ggc cgc gga tga		
	696		
35	Ala Pro Pro Gly Gly Arg Gly		
	225	230	
	<210> 58		
40	<211> 231		
	<212> PRT		
	<213> Unknown		
	<220>		
45	<223> Metagenome - alpha unit nitrile hydratase - M3aG10		
	<400> 58		
	Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr		
50	1	5	10
	5	10	15
	Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His		
	20	25	30
55	Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu		
	35	40	45

Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
 50 55 60

Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
 65 70 75 80

10 Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
 85 90 95

15 Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
 100 105 110

20 Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
 115 120 125

25 Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
 130 135 140

30 Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
 165 170 175

35 His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
 180 185 190

40 Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
 195 200 205

45 Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
 210 215 220

50 Ala Pro Pro Gly Gly Arg Gly
 225 230

55 <210> 59
 <211> 609
 <212> DNA
 <213> Unknown

55 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M73dc9
 <220>
 <221> CDS

<222> (1)..(609)

<223>

<400> 59

5 atg agc tcg aag ccc acc gaa gat ctc ggc acc tac cag ccg ctc acc
48
Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr
1 5 10 15

10 tac tac cag atg atg gaa gtg agc ctg cgc gag ctg ctg gtg gag aag
96
Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys
20 25 30

15 ggc gtg atc acc gaa gcg gaa gtc gcc cgc gcg atg ggc gag atc ggc
144
Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly
35 40 45

20 gcg aga agc ccg gag cgc ggc gcg aag atg gtc gcg cgc gcg tgg gtg
192
Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val
50 55 60

25 gac ccg gcg tac aag gcg cgc atg ctt gcc gac ggc agc aag gcc gcc
240
Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala
65 70 75 80

30 gag gag ctc ggg ttc gag gtg ccg ggc ctc aag ctg atc gtg gtc gag
288
Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu
85 90 95

35 aac acc gcg gac acg cac aac gtg gtc gtg tgc acg ctg tgc tcg tgc
336
Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys
100 105 110

40 tac ccg cgc atc ctg ctc ggc atc ccg ccc gag tgg tac aag tcg cgc
384
Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg
115 120 125

45 agc tac cgc agc cgc aca gtg cgc gag ccg cgc gcg gtg ctc gcc gaa
432
Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu
130 135 140

50 ttc ggc acg acc atc ccg gag aac gtc gcg atc cga gtg cac gac agc
480
Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser
145 150 155 160

55 act gcg gac atg cgc tac ctc gtg atg ccg atg cgg cct gcg ggc acc
528
Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr
165 170 175

gaa aat ttc acc gaa gag cag ctc gct gca ttg gtg acg cgc gac agc
576
Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser
180 185 190
5
ctg atc ggt gtt tcc tta gca acg ctt ccg tag
609
Leu Ile Gly Val Ser Leu Ala Thr Leu Pro
195 200
10
<210> 60
<211> 202
<212> PRT
15 <213> Unknown

<220>
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20 <400> 60

Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr
1 5 10 15
25 Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys
20 25 30

30 Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly
35 40 45

Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val
35 50 55 60

Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala
65 70 75 80
40
Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu
85 90 95

45 Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys
100 105 110

50 Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg
115 120 125

55 Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu
130 135 140

Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser
145 150 155 160

Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr
165 170 175

5

Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser
180 185 190

10

Leu Ile Gly Val Ser Leu Ala Thr Leu Pro
195 200

15 <210> 61
<211> 825
<212> DNA
<213> Unknown

20 <220>
<223> Metagenome - beta unit nitrile hydratase

<220>
<221> CDS
25 <222> (1)..(825)
<223>

<400> 61
atg gtg gga cgt ggg aag tgg gca ctt ggc agt agg cag ttt gct gcg
30 48
Met Val Gly Arg Gly Lys Trp Ala Leu Gly Ser Arg Gln Phe Ala Ala
1 5 10 15

35 gct gcc aac tgg caa ctt atc agt cgc cct tca tgg tca gct tgt aat
96
Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn
20 25 30

40 ata ttg gtc ctc atg agc gcc acg cac ccc aaa aag cgc gcc gcc gac
144
Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp
35 40 45

45 atc ggc ggc aac aaa gcc ggc gcg gtg gac acc gcg gat cac ggc atg
192
Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met
50 55 60

50 aag ttc tgg gag cgg cag gcc aac gcc ctg cgc acc gcg ctg cgg cgc
240
Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg
65 70 75 80

55 aat gga ctg atg agc gta gat gag ctg cgc cgc gca gcg gag gac ctg
288
Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu
85 90 95

gga gac cgc tac gcg aag ctt gag tac ttc gag cgc acg acg ttc gcg
336
Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala
100 105 110

5
ctg cgc acg gtc ctg ctc gaa aag ggc tac ttc acg gag gag tcg ctc
384
Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu
115 120 125

10
gcg gcg aag atg gcc gag gtg cgg aag ccg ctt cga tgt gcc gcg caa
432
Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln
130 135 140

15
gaa gga att gcc ggt gaa gaa gaa agt gaa gcg atg aac cca gcg acg
480
Glu Gly Ile Ala Gly Glu Glu Ser Glu Ala Met Asn Pro Ala Thr
145 150 155 160

20
ggc aag cag gac ggc caa cgg ctg cca tct acg tat acc gcg gcg ccc
528
Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro
165 170 175

25
ggg cac cga ttc gat gtc ggt gac cgc gtt gtg gtc aag cgc tca aat
576
Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn
180 185 190

30
ccg ccc ggc cac cgc cgc acg cct cat tac atc cgc ggc aag acg ggc
624
Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly
195 200 205

35
gtg atc gag cgc atc tgc ggc gcc ttc ccc aac ccg gaa gag ctg gca
672
Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala
210 215 220

40
tac gga ttc gac ggc gaa ccg aag aag gtg ctc tac cgc gtg cga ttc
720
Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe
225 230 235 240

45
cgg caa aaa gag gtg tgg ccg tat cgc ggc ccg gcg cac gac gtg
768
Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val
245 250 255

50
atc gag atg gag att ttc gag cat tgg ctc gag ccg gcg cag agc cag
816
Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln
260 265 270

55
aaa acc tga
825
Lys Thr

5 <210> 62
 <211> 274
 5 <212> PRT
 <213> Unknown

10 <220>
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 10 <400> 62

15 Met Val Gly Arg Gly Lys Trp Ala Leu Gly Ser Arg Gln Phe Ala Ala
 1 5 10 15

20 Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn
 20 25 30

25 Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp
 35 40 45

30 Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met
 50 55 60

35 Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg
 65 70 75 80

40 Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu
 85 90 95

45 Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala
 100 105 110

50 Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu
 115 120 125

55 Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln
 130 135 140

60 Glu Gly Ile Ala Gly Glu Glu Ser Glu Ala Met Asn Pro Ala Thr
 145 150 155 160

65 Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro
 165 170 175

70 Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn
 180 185 190

Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly
195 200 205

5

Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala
210 215 220

10 Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe
225 230 235 240

15 Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val
245 250 255

20 Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln
260 265 270

Lys Thr

25

<210> 63
<211> 627
<212> DNA
<213> Unknown

30

<220>
<223> Metagenome - beta unit nitrile hydratase - M12K24

35

<220>
<221> CDS
<222> (1)..(627)
<223>

<400> 63

40 atg gac ggc atg cac gac ctg gga ggc agg cag ggc ttc gga ccg gtt
48

Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val
1 5 10 15

45

cgc tac acg atc gac gcg ccc gca ttc cat tcg ccg tgg gaa gtg cgc
96

Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg
20 25 30

50

gcg aat tcg ctc tat gcg ttc gcg gtg cgc ctc ggc atc ttc aac atg
144

Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met
35 40 45

55

gac gaa tac cgc cat gcg atc gag cgg atg gag ccg cgc cat tac ctc
192

Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu
50 55 60

ggc gcc ggc tat tac gaa cgc tcg ttg acc ggc ctc gcg acc ttg ctg
240
Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu
65 70 75 80
5
gtc gag aag ggc gtc gtg acg cgc gag gaa ctc gag acc cgg gcg cag
288
Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln
85 90 95
10
ggc cgc tac ccg ctg gcg atg ccc agc gcg cct ggc cgc acc aat gcg
336
Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala
100 105 110
15
cag gca cgc gag cgt ttc cag ccg ggc gac cgg gtt cgc gtc aag gcg
384
Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala
115 120 125
20
gat ttc gtg tcg ggg cac gtg cgg atg ccg gcg tac atc cgc ggc aag
432
Asp Phe Val Ser Gly His Val Arg Met Pro Ala Tyr Ile Arg Gly Lys
130 135 140
25
acc ggc gtg gtc agc gag tcc ccg gac tat ccg ttt ccc gat gcg
480
Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala
145 150 155 160
30
cat gcg cac tcg gtc gat gcc cag gac gag cca acc tac gac gtg cgc
528
His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg
165 170 175
35
ttc cgc agc gag'gat cta tgg ccg gat tcc gcc gat tcc gca ctc gtt
576
Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val
180 185 190
40
cac gtc ggc gta ttc cag agc tac ctc gag cgg gag tcg acg cca gga
624
His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly
195 200 205
45
tag
627
50 <210> 64
<211> 208
<212> PRT
<213> Unknown
55 <220>
<223> Metagenome - beta unit nitrile hydratase - M12K24
<400> 64

Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val
1 5 10 15

5 Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg
20 25 30

10 Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met
35 40 45

15 Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu
50 55 60

20 Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu
65 70 75 80

25 Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln
85 90 95

30 Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala
100 105 110

35 Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala
115 120 125

40 Asp Phe Val Ser Gly His Val Arg Met Pro Ala Tyr Ile Arg Gly Lys
130 135 140

45 Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala
145 150 155 160

50 His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg
165 170 175

55 Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val
180 185 190

60 His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly
195 200 205

<210> 65
<211> 660
55 <212> DNA
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M29M24

<220>
<221> CDS
<222> (1)..(660)
5 <223>

<400> 65
atg aac ggc gtt cat gac atg ggc ggc atg cac ggc atg ggt gcg atc
48
10 Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile
1 5 10 15

cgc cgc gag gag aac gag ccc gct ttc cac gag ccc tgg gag ggg cgg
96
15 Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg
20 25 30

gtt ttc gct ctg acc acg gcg gtc gag gcc tgg ggt cgg tgg acc ctc
144
20 Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu
35 40 45

gat gct tcc cga cac cgg atc gag cgg atg aat gcg gcg gac tat ctg
192
25 Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu
50 55 60

cgg gtg agc tat tac gag aag tgg ctc gag tcg ctt ctc gct ctc ctg
240
30 Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu
65 70 75 80

tcc gag acc gga atg gcg agt ccg gcg gag ata cgg agt ggg gag cgt
288
35 Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg
85 90 95

gcc gac ggc aca ccg aaa gcg acc ccg ccg ctc ccg gcc gac cac gtg
336
40 Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val
100 105 110

acg gcg att ctc gcc agc ggg ttt ccc gcg agc cgg gag gcg gga gct
384
45 Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala
115 120 125

gcg cct cgc ttc cga gtg agc gag cgg gtg cgc acc cgg aac atc aac
432
50 Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn
130 135 140

ccg acg act cac acg cgc ctt ccg cga tac gcc cgg cgg aag ctc ggg
480
55 Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly
145 150 155 160

acg atc gag cgc gac cac gga gtg ttc gtc ttc ccg gat acg aac gcg
528

Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala
165 170 175

5 cac gct ctc ggg gag aaa ccg cag cac gtc tat tcg gtt cgt ttc gag
576 His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu
180 185 190

10 gcg cgt gag ctc tgg ggc gag act gcc agg cca gag gat tcc gtc tac
624 Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr
195 200 205

15 atc gat ctt tgg gac gag tac ctt gaa ccc gtg tag
660 Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val
210 215

20 <210> 66
<211> 219
<212> PRT
<213> Unknown

25 <220>
<223> Metagenome - beta unit nitrile hydratase - M29M24
<400> 66

30 Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile
1 5 10 15

35 Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg
20 25 30

40 Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu
35 40 45

45 Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu
50 55 60

50 Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu
65 70 75 80

55 Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg
85 90 95

60 Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val
100 105 110

65 Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala
115 120 125

Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn
130 135 140

5

Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly
145 150 155 160

10

Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala
165 170 175

15 His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu
180 185 190

20 Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr
195 200 205

25 Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val
210 215

30 <210> 67
<211> 660
<212> DNA
<213> Unknown

35 <220>
<223> Metagenome - beta unit nitrile hydratase - M2K17

40 <400> 67
atg acc aat tcg ctg cac gac atg ggc ggc atg cac ggc ttt ggc cgg
48 Met Thr Asn Ser Leu His Asp Met Gly Gly Met His Gly Phe Gly Arg
1 5 10 15

45 gtc gag ccc gag ccg aac gag ccg ccg ttt cac cag cgc tgg gag ggc
96 Val Glu Pro Glu Pro Asn Glu Pro Pro Phe His Gln Arg Trp Glu Gly
20 25 30

50 cgg gtg ctg ggg atg cag cgc gcc atg ggc ttt acc ggg ctg tgg acc
144 Arg Val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr
35 40 45

55 atc gac gcc ggc cgc gcc tcg ctc gaa gcc ctg ccg cca tta gcg tat
192 Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr
50 55 60

ctg ggt tcg tcc tac tat cgg cgc tgg ttt ctt ggc ctg gag agc cgg
 240
 Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg
 5 65 70 75 80

 ctg ctg ctg cgc ggc ctc gtt ggc gag gac gag atc gcg gca ggc cgt
 288
 Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg
 10 85 90 95

 tcg atg cgc gcc ggc gcc atg ttg ccg cgc acc ctg acc cag gcc gat
 336
 Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp
 15 100 105 110

 gtg gag aaa acc ctg acc cgc ggc gac ttc gcc cgc ccg acc aac acc
 384
 Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr
 20 115 120 125

 ccg gcg cgt ttc cag ccg ggc gac ccg gtg caa acg aag aac atc aac
 432
 Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn
 25 130 135 140

 ccg gcg acc cac acc cgc ctg ccg cgc tat gcc cgc ggc aag act ggc
 480
 Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly
 30 145 150 155 160

 acg gtc gag gcg gtc cgc ggc gtt cac gtc ttt ccc gac acc gcc gcg
 528
 Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala
 35 165 170 175

 ctc ggc gcc ggc gac gac ccg caa tgg ctc tac gcc gtg gtc ttc ccg
 576
 Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro
 40 180 185 190

 gcg cgc gag ttg tgg gga gag gcg gcc gat ccc gcg atc aaa atc tcg
 624
 Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser
 45 195 200 205

 atc gag gcg ttc gaa ccc tat atc gac ccc gca tga
 660
 Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala
 50 210 215

 <210> 68
 <211> 219
 55 <212> PRT
 <213> Unknown

 <220>
 <223> Metagenome - beta unit nitrile hydratase - M2K17

<400> 68

5 Met Thr Asn Ser Leu His Asp Met Gly Gly Met His Gly Phe Gly Arg
1 5 10 15

10 Val Glu Pro Glu Pro Asn Glu Pro Pro Phe His Gln Arg Trp Glu Gly
20 25 30

15 Arg Val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr
35 40 45

20 Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr
50 55 60

25 Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg
65 70 75 80

30 Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg
85 90 95

35 Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp
100 105 110

40 Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr
115 120 125

45 Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn
130 135 140

50 Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly
145 150 155 160

55 Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala
165 170 175

60 Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro
180 185 190

65 Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser
195 200 205

70 Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala
210 215

<210> 69
<211> 663
<212> DNA
<213> Unknown
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<223> Metagenome - beta unit nitrile hydratase - M23dA12
10 <220>
<221> CDS
<222> (1)..(663)
<223>

<400> 69
15 atg gac ggc gtg cac gac atg ggc ggc atg cac ggt ttc ggc aag gtc
48 Met Asp Gly Val His Asp Met Gly Gly Met His Gly Phe Gly Lys Val
1 5 10 15
20 gag ccg gaa gcg aac gag ccc gcc ttc cat gcg gaa tgg gaa ggc cgc
96 Glu Pro Glu Ala Asn Glu Pro Ala Phe His Ala Glu Trp Glu Gly Arg
20 25 30
25 tgc ctc gcg ctc aac cgc gcc atg ggt gcg atc ggc gcc tgg acc atc
144 Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile
35 40 45
30 gat gaa ggc cgt gcc ggc atc gag atc ctg ccg ccg gag att tat ctt
192 Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu
50 55 60
35 ggc agt tcg tac tat gga aaa tgg gcg cgg cgg ctg gag aat atg gtg
240 Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val
65 70 75 80
40 gtc gca cgc ggg ttc gcg ggc gcc gat gaa ctc gcc gcg ggt cgc gca
288 Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala
85 90 95
45 gcg cgt ccc ggc aga tcg gtg aaa cga aag ctt acg gtc gcc gaa gtg
336 Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val
100 105 110
50 ccg cgc acg ctg acg cgc ggt tca ttt ttc cgc gag gca aca aag ccg
384 Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro
115 120 125
55 gca cga ttt gcg gtc ggc gaa cgc gtg cgc acc agg aac att cat ccg
432 Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro
130 135 140

gcg acg cac act cggttgcg cga tat gcg cgc ggc cat gtc ggc gtg
480
Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val
145 150 155 160

5 atc gag gcg atc cgc ggt tgc cac gta ttt ccc gac tcg gtt gcg atc
528
Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile
165 170 175

10 ggc gcc ggc gag aac ccg caa tgg ctt tat acg gtg gtg ttc gaa ggc
576
Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly
180 185 190

15 cgc acg ctg tgg ggc gat agc gcc gat ccg acg ctt aag gtc tcg atc
624
Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile
195 200 205

20 gag gcg ttc gag ccg tat ctg gaa ccg gcc caa cca tga
663
Glu Ala Phe Glu Pro Tyr Leu Glu Pro Ala Gln Pro
210 215 220

25 <210> 70
<211> 220
<212> PRT
30 <213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M23dA12

35 <400> 70

Met Asp Gly Val His Asp Met Gly Gly Met His Gly Phe Gly Lys Val
1 5 10 15

40 Glu Pro Glu Ala Asn Glu Pro Ala Phe His Ala Glu Trp Glu Gly Arg
20 25 30

45 Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile
35 40 45

50 Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu
50 55 60

55 Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val
65 70 75 80

Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala
85 90 95

Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val
100 105 110

5

Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro
115 120 125

10 Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro
130 135 140

15 Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val
145 150 155 160

20 Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile
165 170 175

20

Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly
180 185 190

25

Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile
195 200 205

30 Glu Ala Phe Glu Pro Tyr Leu Glu Pro Ala Gln Pro
210 215 220

35

<210> 71
<211> 888
<212> DNA
<213> Unknown

40

<220>
<223> Metagenome - beta unit nitrile hydratase - M49bD9

45

<220>
<221> CDS
<222> (1)..(888)
<223>

50

<400> 71
atg aac ggc gta cac gat ctt ggc ggg atg gat ggt ttc ggc cgg gtg
48
Met Asn Gly Val His Asp Leu Gly Gly Met Asp Gly Phe Gly Arg Val
1 5 10 15

atg gcg gag gcg gac gag ccg gtc ttt cat gag ccc tgg gaa ggt cgc
96

55

Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg
20 25 30

gtg ttt gcg ctc aac atg ctc ggc atc ggg cgc gag ccc att ccg gtg
144

Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val
35 40 45

5 gac gcg ctg cgc cat cgc att gag cgg atc gag ccg tgg cgc tat ctg
192

Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu
50 55 60

10 acg tcg agc tat tac gaa cga tgg ctg gcc gaa atg gag cag gcc atc
240

Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile
65 70 75 80

15 atc gat gcg ggc acg ctg act cct ggt gaa atc gat gcg cga atg ggc
288

Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly
85 90 95

20 gag ctc gaa acg gat cct gat cgc cca ctg cca agg act gat aac cct
336

Glu Leu Glu Thr Asp Pro Asp Arg Pro Leu Pro Arg Thr Asp Asn Pro
100 105 110

25 gag cat gcc gat ggg gtg gcg gcg ttg cgc gcc ggc agt ccc gta
384

Glu His Ala Asp Gly Val Ala Ala Leu Arg Ala Gly Ser Pro Val
115 120 125

30 acg cgc aag att cgc aag cag ccg cgc ttc aca atc ggc gat cgg gtc
432

Thr Arg Lys Ile Arg Lys Gln Pro Arg Phe Thr Ile Gly Asp Arg Val
130 135 140

35 gta acg cgc aat ctt aat ccg cac ggc cat acg cgg ctg ccg cgc tat
480

Val Thr Arg Asn Leu Asn Pro His Gly His Thr Arg Leu Pro Arg Tyr
145 150 155 160

40 gcg cgc ggc aag cgc ggc gtc gta acg ctg cac cat ggc gca cat gtc
528

Ala Arg Gly Lys Arg Gly Val Val Thr Leu His His Gly Ala His Val
165 170 175

45 ttt ccg gat acg aac gcg cac ggg ctg ggc gag cat ccg cag cat ctc
576

Phe Pro Asp Thr Asn Ala His Gly Leu Gly Glu His Pro Gln His Leu
180 185 190

50 tat acg gtg cga ttt cct gcg cgc gag tta tgg agc gac gcg gcc gag
624

Tyr Thr Val Arg Phe Pro Ala Arg Glu Leu Trp Ser Asp Ala Ala Glu
195 200 205

55 ccg aaa gaa tcg ata atg atc gat ttg tgg gag agc tat ctt caa ccc
672

Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro
210 215 220

gat atc ggc agc aaa gcg tcg tcg tcc gcg aaa ggc aaa gcg acg ccg
720
Asp Ile Gly Ser Lys Ala Ser Ser Ser Ala Lys Gly Lys Ala Thr Pro
225 230 235 240
5
aaa gtt aag ccc gca atg gcc aag gca acc gcc aag gta agc gtc tcg
768
Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser
245 250 255
10
gcc aag gcc aaa act cgg gga aag gcg gcg ccg aag gag cgt cca aaa
816
Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys
260 265 270
15
ctg aaa cct gcg cga gcg gcg acc tca gca gca tcc ggc ggc gaa aaa
864
Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys
275 280 285
20
gct aag cga aag gcc aaa cga tga
888
Ala Lys Arg Lys Ala Lys Arg
290 295
25

<210> 72
<211> 295
<212> PRT
30 <213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M49bD9
35 <400> 72

Met Asn Gly Val His Asp Leu Gly Gly Met Asp Gly Phe Gly Arg Val
1 5 10 15
40
Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg
20 25 30

45 Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val
35 40 45

50 Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu
50 55 60

55 Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile
65 70 75 80
Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly
85 90 95

<223> Metagenome - beta unit nitrile hydratase - M6dE2

<220>

5 <221> CDS

<222> (1)..(630)

<223>

<400> . 73

10 atg gac ggc att cat gat ctc ggt ggg atg agc ggg ttc ggt ctc gtg
48 Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val
1 5 10 15

15 gag atc gag ccc gat gag ccg gtg ttc cac gag ccc tgg gag gcg ctg
96 Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu
20 25 30

20 gtt ttc gct ctg atg act ctc ggt atc ggg aag ctc ggc gcg tac aac
144 Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn
35 40 45

25 gcc gat gag tac cgc cac tcg atc gag cgg atg gat ccg gcc cac tac
192 Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr
50 55 60

30 ctt gcg gcg acg tac tac gag cgc atg ctc acc ggc gtc gca acg ctc
240 Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu
65 70 75 80

35 ctc gtc gag aag aac gtc gtt gcc cgc gac gag ctc gaa gcg cgc gcc
288 Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala
85 90 95

40 ggc ggg ccc ttc ccg ctg tca cgg ccg gtg gcc gag cgg ccg acg gcg
336 Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala
100 105 110

45 gac ctt cgg ccc cag cca caa cca cgc ttc gcg gtc ggg gat cgg gtc
384 Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val
115 120 125

50 gtc gtg cgc gac atc cac ccg gcc ggg cat act cgt gtg ccg cgc tac
432 Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr
130 135 140

55 gtg cgg ggc aag cgc ggg acc gtc gtg cac gtc gcg ccg aaa ttc tcg
480 Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser
145 150 155 160

ttc ccc gac acg gcc gcg cac ggg ctg acc cat cg^g agc gag cac acg
528
Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr
165 170 175

5 tat cac gtg gaa ttc gtc gcg agt gac ctt tgg gcc gac gtg gcc ggg
576
Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly
180 185 190

10 agc aat gag agc gta ctc gtg gac ctg tgg gac ggc tat ctg gag ggc
624
Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly
195 200 205

15 gca tga
630
Ala

20

<210> 74
<211> 209
<212> PRT
25 <213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M6dE2

30 <400> 74

Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val
1 5 10 15

35 Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu
20 25 30

40 Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn
35 40 45

45 Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr
50 55 60

50 Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu
65 70 75 80

Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala
85 90 95

55 Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala
100 105 110

Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val
115 120 125

5 Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr
130 135 140

10 Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser
145 150 155 160

15 Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr
165 170 175

20 Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly
180 185 190

25 Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly
195 200 205

30 Ala

<210> 75

<211> 651

<212> DNA

<213> Unknown

<220>

35 <223> Metagenome - beta unit nitrile hydratase - M25A18

<220>

<221> CDS

<222> (1)..(651)

40 <223>

<400> 75

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48

45 Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp
1 5 10 15

acc gct ccc cac gaa ccg acc ttc tgg gaa aag cag gtg gac gcg atc
96

50 Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile
20 25 30

cac ggc ctg ctc ggc gat tcc aag cgc cgc atc acg ctg cgc gac gag
144

55 His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu
35 40 45

aac cgc ctc tat atc gaa tcg ctc ggc gac gac gtc tac aac acg ctc
192

	Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu	
50	55	60
5	ggc tat tac gag cgc tgg acc gcc gcc atg tgc cgc cag ctc atc gac	
	240	
	Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp	
65	70	75
		80
10	aag ggc gtg ctg acg cag gac gag atc gac gcc aag atc gcc gag ctg	
	288	
	Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu	
	85	90
		95
15	cgc gcc cgc ggc gtc ggc gcg gga cga cga aac ggc ctg caa acc	
	336	
	Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr	
	100	105
		110
20	gtg agc gcc gat ctg gcc gat ctg gcc atc gcg ccg cgc ttc gcc	
	384	
	Val Ser Ala Asp Leu Ala Ala Asp Leu Ala Ile Ala Pro Arg Phe Ala	
	115	120
		125
25	gcc ggc gac cgc gtg cgg gtg cgc gac gat tat ccg ccc ggg cac atc	
	432	
	Ala Gly Asp Arg Val Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile	
	130	135
		140
30	cgc acg ccg gtc tat gtg cgc ggc aag acg ggc gtg gtg acg cgc tgc	
	480	
	Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys	
	145	150
		155
		160
35	ttc ggc gcg ttc aag aac ccg gaa ttg ctc gcc atc ggc aag gac ggc	
	528	
	Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly	
	165	170
		175
40	ctg ccc aag aaa att ctc tac gaa gtg cgc ttc aag cag acc gat ctc	
	576	
	Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu	
	180	185
		190
45	tgg ccc gac tat gcc ggg ccg gcg acc gat acg ctg ctg atc gac atc	
	624	
	Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile	
	195	200
		205
50	tac gaa cat tgg ctg agc gac gcg tga	
	651	
	Tyr Glu His Trp Leu Ser Asp Ala	
	210	215
55	<210> 76	
	<211> 216	
	<212> PRT	
	<213> Unknown	

<220>

<223> Metagenome - beta unit nitrile hydratase - M25A18

<400> 76

5

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1 5 10 1510 Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile
20 25 3015 His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu
35 40 4520 Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu
50 55 60Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp
65 70 75 8025 Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu
85 90 9530 Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr
100 105 11035 Val Ser Ala Asp Leu Ala Ala Asp Leu Ala Ile Ala Pro Arg Phe Ala
115 120 12540 Ala Gly Asp Arg Val Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile
130 135 140Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys
145 150 155 16045 Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly
165 170 17550 Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu
180 185 19055 Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile
195 200 205Tyr Glu His Trp Leu Ser Asp Ala
210 215

5 <210> 77
 <211> 657
 5 <212> DNA
 <213> Unknown

10 <220>
 <223> Metagenome - beta unit nitrile hydratase - M50bD9
10 <220>
 <221> CDS
 <222> (1)..(657)
 <223>

15 <400> 77
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 48
 Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile
20 1 5 10 15
 cag atc gag aag gac gag tcg ccc ttc cat gcg cgc tgg gaa ggc cgg
 96
 Gln Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg
25 20 25 30
 gcg caa gcg atg tac aac gcc att gcg gcc acg ggc aga ctg gtg ctt
 144
 Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu
30 35 40 45
 ggc ggt aga ccc aca cgg gaa ggg ttc ccg ccg gcc gaa tat ctc cgc
 192
 Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg
35 50 55 60
 atg agc tac tat gaa ttg ggt ttc agg gtg ctg gtc gag gac ttg gtc
 240
 Met Ser Tyr Tyr Glu Leu Gly Phe Arg Val Leu Val Glu Asp Leu Val
40 65 70 75 80
 ctg aac ggt ttg gtg acg cgc gcg gaa atc acg agc ggc cgt ccg gca
 288
 Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala
45 85 90 95
 aag ggg gct gca aag tcg acg ccc gca atc acc gcc gcc acc gcg cag
 336
 Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln
50 100 105 110
 gca tat atg ttc gcg ctc aaa tcg acc cgg cga gac gta ccg gtc acg
 384
 Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr
55 115 120 125
 gcg cgt ttc caa gtc ggt cag cgt gtg cgc gcg cgc aac atc aat ccg
 432
 Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro

	130	135	140													
	gtc acc cat acg cgc ctg ccc cgt tac gcg cgc ggc aaa ttc ggc gtt															
	480															
5	Val	Thr	His	Thr	Arg	Leu	Pro	Arg	Tyr	Ala	Arg	Gly	Lys	Phe	Gly	Val
	145				150					155					160	
	atc gaa cgt gac cac ggt gtt tac agg ttc gac gat tcc ttt gcc acg															
	528															
10	Ile	Glu	Arg	Asp	His	Gly	Val	Tyr	Arg	Phe	Asp	Asp	Ser	Phe	Ala	Thr
					165				170					175		
	tcc ggc gac gag aag ccc cag cac gtt tat tct gtg cgc ttc gcg gcg															
	576															
15	Ser	Gly	Asp	Glu	Lys	Pro	Gln	His	Val	Tyr	Ser	Val	Arg	Phe	Ala	Ala
					180				185				190			
	cgc gaa cta tgg ggc gaa gcc gcg ccg cga gat gct gtc tat atc															
	624															
20	Arg	Glu	Leu	Trp	Gly	Glu	Ala	Ala	Pro	Pro	Arg	Asp	Ala	Val	Tyr	Ile
					195			200			205					
	gaa atc tgg gat gac aac ctt gag cca gcg tga															
	657															
25	Glu	Ile	Trp	Asp	Asp	Asn	Leu	Glu	Pro	Ala						
					210			215								
	<210> 78															
30	<211>	218														
	<212>	PRT														
	<213>	Unknown														
	<220>															
35	<223>	Metagenome - beta unit nitrile hydratase - M50bD9														
	<400> 78															
	Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile															
40	1	5	10	15												
	Gln Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg															
	20		25	30												
45																
	Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu															
	35		40	45												
50																
	Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg															
	50	55	60													
55	Met	Ser	Tyr	Tyr	Glu	Leu	Gly	Phe	Arg	Val	Leu	Val	Glu	Asp	Leu	Val
	65				70					75			80			
	Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala															

85 90 95

5 Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln
100 105 110

10 Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr
115 120 125

15 Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro
130 135 140

20 Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val
145 150 155 160

25 Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr
165 170 175

30 Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala
180 185 190

35 Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile
195 200 205

40 Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala
210 215

45 <210> 79
<211> 696
<212> DNA
<213> Unknown

50 <220>
<223> Metagenome - beta unit nitrile hydratase - M3aG10

55 <220>
<221> CDS
<222> (1)..(696)
<223>

50 atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc
48 48
Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr
1 5 10 15

55 ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac
96 96
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His
20 25 30

cag cat caa gat ttg ccg tcc gat ctg gcg ctg cggt aag tcg ctc
144
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu
35 40 45

5
gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac
192
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
50 55 60

10
gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg
240
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
65 70 75 80

15
cgc gtt gtc gcg cggt gcc tgg gtt gac ccg gac tac aag caa cgg tta
288
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
85 90 95

20
ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg
336
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
100 105 110

25
cag ggc gct gac atc cggt gtc gaa aac acg gcc act gta cat aac
384
Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
115 120 125

30
ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc
432
Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
130 135 140

35
ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg
480
Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val
145 150 155 160

40
atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac
528
Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
165 170 175

45
cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta
576
His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
180 185 190

50
gtg ctg ccg gag ccg gcc gga acc aac ctg aca gaa gaa gcg
624
Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
195 200 205

55
ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc
672
Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
210 215 220

gct ccg ccg gga ggc cgc gga tga
696
Ala Pro Pro Gly Gly Arg Gly
5 225 230

<210> 80
<211> 231
10 <212> PRT
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M3aG10
15 <400> 80

Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr
1 5 10 15

20 Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His
20 25 30

25 Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu
35 40 45

30 Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
50 55 60

35 Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
65 70 75 80

40 Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
85 90 95

Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
100 105 110

45 Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
115 120 125

50 Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
130 135 140

55 Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val
145 150 155 160

Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
165 170 175

His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
180 185 190

5

Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
195 200 205

10

Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
210 215 220

15 Ala Pro Pro Gly Gly Arg Gly
225 230

20 <210> 81
<211> 327
<212> DNA
<213> Unknown

25 <220>
<223> Metagenome - p12K unit

30 <220>
<221> CDS
<222> (1)..(327)
<223>

35 <400> 81
atg aaa gat agc ccg gtc ttt cgc gag ccg tgg gaa gcg cag gcg ttt
48

Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe
1 5 10 15

gcg ttg gcg atc tcg ttg caa gac cgt ggc gtg ttc acg cga gac gaa
96

40 Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu
20 25 30

tgg gcg gcg gca ctc ggc gat gaa atc aag aag gcg caa gct gcc ggc
144

45 Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly
35 40 45

gat ccc gat acg ggc gag act tat tac cat cat tgg atg gca gcg ctc
192

50 Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu
50 55 60

gaa cgg ctg att gca gcc aag ggt gtt gcc gat acg cag acg ctc gcg
240

55 Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala
65 70 75 80

cgc aca cgc gac gcc tgg cag cac gcc tgt gcg cga acg ccg cat ggc
288

Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly
85 90 95

5 gcg cca atc gag cta aga ccg gac gac ttc agg aat tga
327 Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn
100 105

10 <210> 82
<211> 108
<212> PRT
<213> Unknown

15 <220>
<223> Metagenome - p12K unit

<400> 82

20 Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe
1 5 10 15

25 Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu
20 25 30

30 Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly
35 40 45

Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu
50 55 60

35 Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala
65 70 75 80

40 Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly
85 90 95

45 Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn
100 105

50 <210> 83
<211> 321
<212> DNA
<213> Unknown

55 <220>
<223> Metagenome - p12K unit

<220>
<221> CDS
<222> (1)..(321)
<223>

<400> 83
atg aga aca gtt gct gag caa atc gcg gct gat ctt gcg agt ccg gcg
48
5 Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala
1 5 10 15
gcg att ccg cgc cgc aac ggc gag ccg gtc ttc gac gag cct tgg gaa
96
10 Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu
20 25 30
agt cgt gcg ttt ggg ata gcg gtc gcc ctt tcc gag ggt ggc ctc tat
144
15 Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr
35 40 45
tca tgg gat gaa ttt cgc gat tgc ctg att gct gaa atc aca gcg gcg
192
20 Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala
50 55 60
gat gcg cgc ggc gag cat acg agc tat tac gaa cgg ttt ctc gcc gcc
240
25 Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala
65 70 75 80
ctg cag cat ctg ctc gcg gcc aaa cgc ctc tgc act ccc gat gaa gtc
288
30 Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val
85 90 95
gag cgg cgg atg aac act agc gca ggc acc tga
321
35 Glu Arg Arg Met Asn Thr Ser Ala Gly Thr
100 105

<210> 84
40 <211> 106
<212> PRT
<213> Unknown

<220>
45 <223> Metagenome - p12K unit

<400> 84

Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala
50 1 5 10 15
Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu
20 25 30
55 Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr
35 40 45

50 Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala
55. 60

5

Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala
65 70 75 80

10 Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val
85 90 95

15 Glu Arg Arg Met Asn Thr Ser Ala Gly Thr
100 105

<210> 85

<211> 426

20 <212> DNA

<213> Unknown

<220>

<223> Metagenome - p12K unit

25

<220>

<221> CDS

<222> (1)..(426)

<223>

30

<400> 85

atg aca acc ttg agc cag cgt gaa gcg gcc ccc tcg gcc gag ctt ctt
48

35 Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu
1 5 10 15

gac cta ccg caa ctt cca agc gac acc gac ggc ccc gtc ttc gcg gaa
96

40 Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu
20 25 30

cct tgg gaa gcg gaa gcg ttt gcg ctt gcc gta agt ctt tca gag caa
144

45 Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln
35 40 45

gga cat ttc acg tgg aag gaa tgg gca gca acg ctc gcc gat gaa ctg
192

50 Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu
50 55 60

gag ggc gcc gcc aat cgc ggc gag ccg gat gac ggt acg cat tat tat
240

55 Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr
65 70 75 80

gag tac tgg ctg acg gcc ctg gaa agg ctg gtt acg atc aag ggc ctg
288

Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu

	85	90	95
	aca gat cag caa gcg atg cgc gag cgc aaa gag gcg tgg gaa gaa gcc		
	336		
5	Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala		
	100	105	110
	tat cgc cat acc ccg cat ggc gcg cca gtt gaa ctt atg tct ccg ctc		
	384		
10	Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu		
	115	120	125
	gat caa agc cgg ata gcc gaa gag gac agc gaa tcc tca tag		
	426		
15	Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser		
	130	135	140
	<210> 86		
20	<211> 141		
	<212> PRT		
	<213> Unknown		
	<220>		
25	<223> Metagenome - p12K unit		
	<400> 86		
30	Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu		
	1	5	10
			15
	Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu		
	20	25	30
35	Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln		
	35	40	45
40	Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu		
	50	55	60
45	Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr		
	65	70	75
			80
50	Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu		
	85	90	95
	Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala		
	100	105	110
55	Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu		
	115	120	125

Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser
130 135 140